

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/526,073A
Source: 1FWO
Date Processed by STIC: 8/28/06

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 08/28/2006

PATENT APPLICATION: US/10/526,073A

TIME: 08:53:29

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\08282006\J526073A.raw

3 <110> APPLICANT: TAKARA BIO INC.
 4 HOKAZONO, Shigekazu
 5 UEMORI, Takashi
 6 TANAKA, Tetsuki
 7 KATO, Ikunoshin
 9 <120> TITLE OF INVENTION: Thermostable RNase H
 11 <130> FILE REFERENCE: HOKAZONO1
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/526,073A
 14 <141> CURRENT FILING DATE: 2005-02-28
 16 <150> PRIOR APPLICATION NUMBER: JP 2002-254153
 17 <151> PRIOR FILING DATE: 2002-08-30
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP03/10727
 20 <151> PRIOR FILING DATE: 2003-08-26
 22 <160> NUMBER OF SEQ ID NOS: 16
 24 <170> SOFTWARE: PatentIn version 3.3
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 211
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Archaeoglobus profundus
 31 <400> SEQUENCE: 1
 33 Met Ile Ala Gly Ile Asp Glu Ala Gly Lys Gly Pro Val Ile Gly Pro
 34 1 5 10 15
 37 Leu Val Ile Cys Gly Val Leu Cys Asp Glu Glu Thr Val Glu Tyr Leu
 38 20 25 30
 41 Lys Ser Val Gly Val Lys Asp Ser Lys Lys Leu Asp Arg Arg Lys Arg
 42 35 40 45
 45 Glu Glu Leu Tyr Asn Ile Ile Lys Ser Leu Cys Lys Val Lys Val Leu
 46 50 55 60
 49 Lys Ile Ser Val Glu Asp Leu Asn Arg Leu Met Glu Tyr Met Ser Ile
 50 65 70 75 80
 53 Asn Glu Ile Leu Lys Arg Ala Tyr Val Glu Ile Ile Arg Ser Leu Met
 54 85 90 95
 57 Pro Lys Val Val Tyr Ile Asp Cys Pro Asp Ile Asn Val Glu Arg Phe
 58 100 105 110
 61 Lys His Glu Ile Glu Glu Arg Thr Gly Val Glu Val Phe Ala Ser His
 62 115 120 125
 65 Lys Ala Asp Glu Ile Tyr Pro Ile Val Ser Ile Ala Ser Ile Val Ala
 66 130 135 140
 69 Lys Val Glu Arg Asp Phe Glu Ile Asp Lys Leu Lys Lys Ile Tyr Gly
 70 145 150 155 160
 73 Asp Phe Gly Ser Gly Tyr Pro Ser Asp Leu Arg Thr Ile Glu Phe Leu
 74 165 170 175
 77 Arg Ser Tyr Leu Arg Glu His Lys Ser Phe Pro Pro Ile Val Arg Lys

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78          180          185          190
81 Arg Trp Lys Thr Leu Lys Arg Leu Thr Thr His Thr Leu Ser Asp Phe
82          195          200          205
85 Phe Glu Val
86          210
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 636
91 <212> TYPE: PRT
92 <213> ORGANISM: Archaeoglobus profundus
94 <400> SEQUENCE: 2
96 Ala Thr Gly Ala Thr Thr Gly Cys Thr Gly Gly Gly Ala Thr Ala Gly
97 1          5          10          15
100 Ala Cys Gly Ala Ala Gly Cys Thr Gly Gly Ala Ala Ala Ala Gly Gly
101          20          25          30
104 Ala Cys Cys Thr Gly Thr Ala Ala Thr Ala Gly Gly Cys Cys Cys Thr
105          35          40          45
108 Cys Thr Thr Gly Thr Ala Ala Thr Ala Thr Gly Cys Gly Gly Ala Gly
109          50          55          60
112 Thr Ala Cys Thr Gly Thr Gly Cys Gly Ala Thr Gly Ala Ala Gly Ala
113 65          70          75          80
116 Gly Ala Cys Cys Gly Thr Ala Gly Ala Ala Thr Ala Cys Thr Thr Gly
117          85          90          95
120 Ala Ala Gly Ala Gly Cys Gly Thr Ala Gly Gly Cys Gly Thr Thr Ala
121          100          105          110
124 Ala Ala Gly Ala Thr Thr Cys Ala Ala Ala Gly Ala Ala Gly Cys Thr
125          115          120          125
128 Gly Gly Ala Thr Ala Gly Gly Ala Gly Gly Ala Ala Gly Ala Gly Ala
129          130          135          140
132 Gly Ala Gly Gly Ala Ala Cys Thr Thr Thr Ala Cys Ala Ala Thr Ala
133 145          150          155          160
136 Thr Cys Ala Thr Ala Ala Ala Ala Thr Cys Gly Cys Thr Thr Thr Gly
137          165          170          175
140 Cys Ala Ala Gly Gly Thr Thr Ala Ala Gly Gly Thr Ala Thr Thr Gly
141          180          185          190
144 Ala Ala Ala Ala Thr Ala Thr Cys Thr Gly Thr Cys Gly Ala Gly Gly
145          195          200          205
148 Ala Thr Thr Thr Gly Ala Ala Cys Ala Gly Gly Thr Thr Ala Ala Thr
149          210          215          220
152 Gly Gly Ala Ala Thr Ala Cys Ala Thr Gly Ala Gly Thr Ala Thr Ala
153 225          230          235          240
156 Ala Ala Thr Gly Ala Ala Ala Thr Cys Thr Thr Gly Ala Ala Gly Ala
157          245          250          255
160 Gly Ala Gly Cys Thr Thr Ala Cys Gly Thr Thr Gly Ala Ala Ala Thr
161          260          265          270
164 Ala Ala Thr Ala Ala Gly Gly Thr Cys Thr Thr Thr Gly Ala Thr Gly
165          275          280          285
168 Cys Cys Thr Ala Ala Ala Gly Thr Thr Gly Thr Gly Thr Ala Cys Ala
169          290          295          300
172 Thr Ala Gly Ala Cys Thr Gly Thr Cys Cys Ala Gly Ala Thr Ala Thr

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173 305          310          315          320
176 Thr Ala Ala Thr Gly Thr Gly Gly Ala Gly Ala Gly Ala Thr Thr Thr
177          325          330          335
180 Ala Ala Gly Cys Ala Cys Gly Ala Ala Thr Ala Gly Ala Gly Gly
181          340          345          350
184 Ala Gly Ala Gly Ala Ala Cys Gly Gly Ala Gly Thr Gly Gly Ala
185          355          360          365
188 Gly Gly Thr Ala Thr Thr Thr Gly Cys Gly Ala Gly Cys Cys Ala Thr
189          370          375          380
192 Ala Ala Ala Gly Cys Gly Gly Ala Cys Gly Ala Gly Ala Thr Ala Thr
193 385          390          395          400
196 Ala Thr Cys Cys Ala Ala Thr Ala Gly Thr Ala Thr Cys Thr Ala Thr
197          405          410          415
200 Ala Gly Cys Thr Thr Cys Gly Ala Thr Ala Gly Thr Cys Gly Cys Ala
201          420          425          430
204 Ala Ala Ala Gly Thr Thr Gly Ala Ala Ala Gly Gly Gly Ala Thr Thr
205          435          440          445
208 Thr Thr Gly Ala Ala Ala Thr Ala Gly Ala Cys Ala Ala Gly Cys Thr
209          450          455          460
212 Gly Ala Ala Gly Ala Ala Gly Ala Thr Thr Thr Ala Thr Gly Gly Ala
213 465          470          475          480
216 Gly Ala Cys Thr Thr Gly Gly Gly Ala Gly Thr Gly Gly Ala Thr
217          485          490          495
220 Ala Thr Cys Cys Ala Thr Cys Ala Gly Ala Thr Cys Thr Ala Ala Gly
221          500          505          510
224 Ala Ala Cys Cys Ala Thr Cys Gly Ala Ala Thr Thr Thr Thr Thr Ala
225          515          520          525
228 Ala Gly Gly Ala Gly Thr Thr Ala Thr Cys Thr Ala Ala Gly Gly Gly
229          530          535          540
232 Ala Ala Cys Ala Cys Ala Ala Ala Ala Gly Thr Thr Thr Thr Cys Cys
233 545          550          555          560
236 Ala Cys Cys Ala Ala Thr Cys Gly Thr Ala Ala Gly Ala Ala Ala Gly
237          565          570          575
240 Ala Gly Ala Thr Gly Gly Ala Ala Ala Ala Cys Thr Cys Thr Cys Ala
241          580          585          590
244 Ala Ala Ala Gly Ala Thr Thr Gly Ala Cys Ala Ala Cys Gly Cys Ala
245          595          600          605
248 Cys Ala Cys Thr Thr Thr Ala Ala Gly Cys Gly Ala Thr Thr Thr Cys
249          610          615          620
252 Thr Thr Thr Gly Ala Ala Gly Thr Thr Thr Ala Gly
253 625          630          635
256 <210> SEQ ID NO: 3
257 <211> LENGTH: 23
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial
261 <220> FEATURE:
262 <223> OTHER INFORMATION: synthetic
265 <220> FEATURE:
266 <221> NAME/KEY: misc_feature

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267 <223> OTHER INFORMATION: PCR primer RN-F1 for cloning a gene encoding a polypeptide
having
268     a RNaseH activity from Archaeoglobus profundus
270 <220> FEATURE:
271 <221> NAME/KEY: misc_feature
272 <222> LOCATION: (18)..(18)
273 <223> OTHER INFORMATION: n is a, c, g, or t
275 <400> SEQUENCE: 3
W--> 276 ggcattgatg aggctggnar rgg                                23
279 <210> SEQ ID NO: 4
280 <211> LENGTH: 20
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial
284 <220> FEATURE:
285 <223> OTHER INFORMATION: synthetic
288 <220> FEATURE:
289 <221> NAME/KEY: misc_feature
290 <223> OTHER INFORMATION: PCR primer RN-R2 for cloning a gene encoding a polypeptide
having
291     a RNaseH activity from Archaeoglobus profundus
293 <220> FEATURE:
294 <221> NAME/KEY: misc_feature
295 <222> LOCATION: (18)..(18)
296 <223> OTHER INFORMATION: n is a, c, g, or t
298 <400> SEQUENCE: 4
W--> 299 ggtagggaaa gctgraancg                                20
302 <210> SEQ ID NO: 5
303 <211> LENGTH: 22
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial
307 <220> FEATURE:
308 <223> OTHER INFORMATION: synthetic
311 <220> FEATURE:
312 <221> NAME/KEY: misc_feature
313 <223> OTHER INFORMATION: PCR primer AprRN-1 for cloning a gene encoding a polypeptide
314     having a RNaseH activity from Archaeoglobus profundus
316 <400> SEQUENCE: 5
317 ctcttcacgcg cacagtactc cg                                22
320 <210> SEQ ID NO: 6
321 <211> LENGTH: 22
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial
325 <220> FEATURE:
326 <223> OTHER INFORMATION: synthetic
329 <220> FEATURE:
330 <221> NAME/KEY: misc_feature
331 <223> OTHER INFORMATION: PCR primer AprRN-2 for cloning a gene encoding a polypeptide
332     having a RNaseH activity from Archaeoglobus profundus
334 <400> SEQUENCE: 6
335 tttgcgagcc ataaagcgga cg                                22
338 <210> SEQ ID NO: 7

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RAW SEQUENCE LISTING

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Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\08282006\J526073A.raw

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339 <211> LENGTH: 17
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial
343 <220> FEATURE:
344 <223> OTHER INFORMATION: synthetic
347 <220> FEATURE:
348 <221> NAME/KEY: misc_feature
349 <223> OTHER INFORMATION: Tag sequence
351 <400> SEQUENCE: 7
352 ggcacgattc gataacg 17
355 <210> SEQ ID NO: 8
356 <211> LENGTH: 39
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial
360 <220> FEATURE:
361 <223> OTHER INFORMATION: synthetic
364 <220> FEATURE:
365 <221> NAME/KEY: misc_feature
366 <223> OTHER INFORMATION: PCR primer AprNde for amplifying a gene encoding a
polypeptide
367     having a RNaseH activity from Archaeoglobus profundus
369 <400> SEQUENCE: 8
370 aatcgatggt gttcatatga ttgctgggat agacgaagc 39
373 <210> SEQ ID NO: 9
374 <211> LENGTH: 39
375 <212> TYPE: DNA
376 <213> ORGANISM: Artificial
378 <220> FEATURE:
379 <223> OTHER INFORMATION: synthetic
382 <220> FEATURE:
383 <221> NAME/KEY: misc_feature
384 <223> OTHER INFORMATION: PCR primer AprBam for amplifying a gene encoding a
polypeptide
385     having a RNaseHIII activity from Archaeoglobus profundus
387 <400> SEQUENCE: 9
388 gcccacgccc tgggatccct aggctacggg tcctttaag 39
391 <210> SEQ ID NO: 10
392 <211> LENGTH: 560
393 <212> TYPE: DNA
394 <213> ORGANISM: Hepatitis B virus
396 <400> SEQUENCE: 10
397 ccttcccatg gctgctcggg tgtgctgcc actggatcct gcgcgggacg tcctttgtct 60
399 acgtcccgtc ggcgctgaat cccgcggacg acccgctctcg gggccgtttg ggccctctacc 120
401 gtcccttgtc ttctctgccg ttccagccga ccacggggcg cacctctctt tacgcggtct 180
403 ccccgctctgt gcctttctcat ctgccggacc gtgtgcactt cgcttcacct ctgcacgtcg 240
405 catggagacc accgtgaacg gccaccaggt cttgcccag ctcttacata agaggactct 300
407 tggactctca gcaatgtcaa caaccgacct tgaggcatac ttcaaagact gtttgtttaa 360
409 agactgggag gagttggggg aggagattag gttaaaggctc tttgtactag gaggctgtag 420
411 gcataaattg gtctgttcac cagcaccatg caacttttct acctctgcct aatcatctca 480
413 tgttcatgtc ctactgttca agcctccaag ctgtgccttg ggtggctttg gggcatggac 540
415 attgaccctg ataaagaatt 560

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/28/2006
PATENT APPLICATION: US/10/526,073A TIME: 08:53:30

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\08282006\J526073A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 18
Seq#:4; N Pos. 18

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,11,12,13,14,15,16

VERIFICATION SUMMARY

DATE: 08/28/2006

PATENT APPLICATION: US/10/526,073A

TIME: 08:53:30

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\08282006\J526073A.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0

L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0